

AMENDMENTS TO THE SPECIFICATION

Please delete the sequence listing from the English translation of the international application and replace it with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the title and before line 4, please insert the following new paragraphs:

RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2005/002734 filed March 15, 2005, which claims benefit of European application 04006358.8 filed March 17, 2004.

SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc, each containing: file name: Final Sequence List-13987-00022-US, date recorded: September 14, 2006, size: 102 KB.

In the specification at page 9 line 34, please replace the paragraph starting with “The D-amino acid” with the following amended paragraph:

The D-amino acid oxidase expressed from the DNA-construct of the invention has preferably metabolising activity against at least one D-amino acid and comprises a sequences motive having the following consensus sequence (SEQ ID NO: 17):

In the specification at page 33 line 14, please replace the paragraph starting with “In DAAO” with the following amended paragraph:

In DAAO, a conserved histidine has been shown (Miyano M et al. (1991) J Biochem 109:171-177) to be important for the enzyme's catalytic activity. In a preferred embodiment of the invention a DAAO is referring to a protein comprising the following consensus motive (SEQ ID NO: 17):

In the specification at page 49 line 12, please replace Table 4 with the following amended Table 4:

Recombi-nase	Organism of origin	Recombination Sites	<u>SEQ ID NO:</u>
CRE	Bacteriophage P1	5'-AACTCTCATCGCTTCGGATAACTTCCTGTTATCCGAAA CATATCACTCACTTTGGTGATTTCACCGTAACT- GTCTATGATTAATG-3'	<u>18</u>
FLP	Saccharomyces cerevisiae	5'-GAAGTTCCTATTCCGAAGTTCCTATTCTCTAGAA AG- TATAGGAACTTC-3'	<u>19</u>
R	pSR1 Plasmids	5'-CGAGATCATATCACTGTGGACGTTGATGAAAGAATAC GTTATTCTTTCATCAAATCGT	<u>20</u>

In the specification starting at page 56 through to page 59, please replace Table 5 with the following amended Table 5:

DSBI Enzyme	Organism of origin	Recognition sequence	<u>SEQ ID NO:</u>
P-Element Transposase	Drosophila	5'-CTAGATGAAATAACATAAGGTGG	<u>21</u>
I-Anil	Aspergillus nidulans	5'-TTGAGGAGGTT^TCTCTGTAAATAANNNNNNNNNNNNNNN 3'-AACTCCTCCAAAGAGACATTTATTNNNNNNNNNNNNNNNN^	<u>22</u>
I-Ddil	Dictyostelium discoideumAX3	5'-TTTTTTGGTCATCCAGAAGTATAT 3'-AAAAAACCAG^TAGGTCTTCATATA	<u>23</u>
I-Cvul	Chlorella vulgaris	5'-CTGGGTTCAAACGTCGTGA^GACAGTTTGG 3'-GACCCAAGTTTGCAG^CACTCTGTCAAACC	<u>24</u>
I-Csml	Chlamydomonas smithii	5'-GTACTAGCATGGGGTCAAATGTCTTTCTGG	<u>25</u>

DSBI Enzyme	Organism of origin	Recognition sequence	SEQ ID NO :
I-Cmoel	Chlamydomonas moewusii	5'-TCGTAGCAGCT^CACGGTT 3'-AGCATCG^TCGAGTGCCAA	<u>26</u>
I-Crel	Chlamydomonas reinhardtii	5'-CTGGGTTCAAACGTCGTGA^GACAGTTTGG 3'-GACCCAAGTTTTGCAG^CACTCTGTCAAACC	<u>27</u>
I-Chul	Chlamydomonas humicola	5'-GAAGGTTTGGCACCTCG^ATGTCGGCTCATC 3'-CTTCCAAACCGTG^GAGCTACAGCCGAGTAG	<u>28</u>
I-Cpal	Chlamydomonas pallidostigmatica	5'-CGATCCTAAGGTAGCGAA^ATTCA 3'-GCTAGGATTCCATC^GCTTTAAGT	<u>29</u>
I-Cpall	Chlamydomonas pallidostigmatica	5'-CCCGGCTAACTC^TGTGCCAG 3'-GGGCCGAT^TGAGACACGGTC	<u>30</u>
I-Ceul	Chlamydomonas eugametos	5'-CGTAACTATAACGGTCCTAA^GGTAGCGAA 3'-GCATTGATATTGCCAG^GATTCCATCGCTT	<u>31</u>
I-Dmol	Desulfuro- coccus mobilis	5'-ATGCCTTGCCGGGTAA^GTTCCGGCGCGCAT 3'-TACGGAACGGCC^CATTCAAGGCCGCGCGTA	<u>32</u>
I-Scel	Saccharomyces cerevisiae	5'-AGTTACGCTAGGGATAA^CAGGGTAATATAG 3'-TCAATGCGATCCC^TATTGTCCCATTATATC 5'-TAGGGATAA^CAGGGTAAT 3'-ATCCC^TATTGTCCCATT ("Core"-Sequence)	<u>33</u> <u>34</u>
I-Scell	S.cerevisiae	5'-TTTTGATTCTTTGGTCACCC^TGAAGTATA 3'-AAAATAAGAAACCAG^TGGGACTTCATAT	<u>35</u>
I-Scelll	S.cerevisiae	5'-ATTGGAGGTTTTGGTAAC^TATTTATTACC 3'-TAACCTCCAAAACC^ATTGATAAATAATGG	<u>36</u>
I-ScelV	S.cerevisiae	5'-TCTTTTCTCTTGATTA^GCCCTAATCTACG 3'-AGAAAAGAGAAC^TAATCGGGATTAGATGC	<u>37</u>
I-SceV	S.cerevisiae	5'-AATAATTTTCT^TCTTAGTAATGCC 3'-TTATTAAGAAGAATCATTAC^CGG	<u>38</u>
I-SceVI	S.cerevisiae	5'-GTTATTTAATG^TTTGTAGTAGTTGG 3'-CAATAAATTACAAAATCATCA^ACC	<u>39</u>
I-SceVII	S.cerevisiae	5'-TGTCACATTGAGGTGCACTAGTTATTAC	<u>40</u>
PI-Scel	S.cerevisiae	5'-ATCTATGTCGGGTGC^GGAGAAAGAGGTAAT 3'-TAGATACAGCC^CACGCCTCTTTCTCCATTA	<u>41</u>
F-Scel	S.cerevisiae	5'-GATGCTGTAGGC^ATAGGCTTGGTT 3'-CTACGACA^TCCGTATCCGAACCAA	<u>42</u>
F-Scell	S.cerevisiae	5'-CTTTCCGCAACA^GTAAAATT 3'-GAAAGGCG^TTGTCATTTTAA	<u>43</u>
I-Hmul	Bacillus subtilis bacteriophage SPO1	5'-AGTAATGAGCCTAACGCTCAGCAA 3'-TCATTACTCGGATTGC^GAGTCGTT	<u>44</u>

DSBI Enzyme	Organism of origin	Recognition sequence	SEQ ID NO.:
I-Hmull	Bacillus subtilis bacteriophage SP82	5'-AGTAATGAGCCTAACGCTCAACAANNNNNNNNNNNNNNNNNN- NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	<u>45</u>
I-Llal	Lactococcus lactis	5'-CACATCCATAAC^CATATCATTTTT 3'-GTGTAGGTATTGGTATAGTAA^AAA	<u>46</u>
I-Msol	Monomastix species	5'-CTGGGTTCAAACGTCGTGA^GACAGTTTGG 3'-GACCCAAGTTTTGCAG^CACTCTGTCAAACC	<u>47</u>
I-Nanl	Naegleria andersoni	5'-AAGTCTGGTGCCA^GCACCCGC 3'-TTCAGACC^ACGGTCGTGGGCG	<u>48</u>
I-Nitl	Naegleria italica	5'-AAGTCTGGTGCCA^GCACCCGC 3'-TTCAGACC^ACGGTCGTGGGCG	<u>49</u>
I-Njal	Naegleria jamiesoni	5'-AAGTCTGGTGCCA^GCACCCGC 3'-TTCAGACC^ACGGTCGTGGGCG	<u>50</u>
I-Pakl	Pseudendoclonium akinetum	5'-CTGGGTTCAAACGTCGTGA^GACAGTTTGG 3'-GACCCAAGTTTTGCAG^CACTCTGTCAAACC	<u>51</u>
I-Porl	Pyrobaculum organotrophum	5'-GCGAGCCCGTAAGGGT^GTGTACGGG 3'-CGCTCGGGCATT^CCCACACATGCC	<u>52</u>
I-Ppol	Physarum polycephalum	5'-TAACTATGACTCTCTTAA^GGTAGCCAAAT 3'-ATTGATACTGAGAG^AATTCCATCGGTTTA	<u>53</u>
I-Scal	Saccharomyces capensis	5'-TGTCACATTGAGGTGCACT^AGTTATTAC 3'-ACAGTGTAACCTCCAC^GTGATCAATAATG	<u>54</u>
I- Ssp6803l	Synechocystis species	5'-GTCGGGCT^CATAACCCGAA 3'-CAGCCCGAGTA^TTGGGCTT	<u>55</u>
PI-Pful	Pyrococcus furiosus Vc1	5'-GAAGATGGGAGGAGGG^ACCGGACTCAACTT 3'-CTTCTACCCTCC^TCCCTGGCCTGAGTTGAA	<u>56</u>
PI-Pfull	Pyrococcus furiosus Vc1	5'-ACGAATCCATGTGGAGA^AGAGCCTCTATA 3'-TGCTTAGGTACAC^CTCTTCTCGGAGATAT	<u>57</u>
PI-Pkol	Pyrococcus kodakaraensis KOD1	5'-GATTTTAGAT^CCCTGTACC 3'-CTAAAA^TCTAGGGACATGG	<u>58</u>
PI-Pkoll	Pyrococcus kodakaraensis KOD1	5'-CAGTACTACG^GTTAC 3'-GTCATG^ATGCCAATG	<u>59</u>
PI-Pspl	Pyrococcus sp.	5'-AAAATCCTGGCAAACAGCTATTAT^GGGTAT 3'-TTTTAGGACCGTTTGTGAT^AATACCCATA	<u>60</u>

DSBI Enzyme	Organism of origin	Recognition sequence	SEQ ID NO :
PI-Tful	<i>Thermococcus fumicolans</i> ST557	5'-TAGATTTTAGGT^CGCTATATCCTTCC 3'-ATCTAAAA^TCCAGCGATATAGGAAGG	<u>61</u>
PI-Tfull	<i>Thermococcus fumicolans</i> ST557	5'-TAYGCNGAYACN^GACGGYTTYT 3'-ATRCGNCT^RTGNCTGCCRAARA	<u>62</u>
PI-Thyl	<i>Thermococcus hydrothermalis</i>	5'-TAYGCNGAYACN^GACGGYTTYT 3'-ATRCGNCT^RTGNCTGCCRAARA	<u>62</u>
PI-Tlil	<i>Thermococcus litoralis</i>	5'-TAYGCNGAYACNGACGG^YTTYT 3'-ATRCGNCTRTGNC^TGCCRAARA	<u>62</u>
PI-TlilI	<i>Thermococcus litoralis</i>	5'-AAATTGCTTGCAAACAGCTATTACGGCTAT	<u>63</u>
I-TevI	Bacteriophage T4	5'-AGTGGTATCAAC^GCTCAGTAGATG 3'-TCACCATAGT^TGCGAGTCATCTAC	<u>64</u>
I-TevII	Bacteriophage T4	5'-GCTTATGAGTATGAAGTGAACACGT^TATTC 3'-CGAATACTCATACTTCACTTGTG^CAATAAG	<u>65</u>
F-TevI	Bacteriophage T4	5'-GAAACACAAGA^AATGTTTAGTAAANNNNNNNNNNNNNN 3'-CTTTGTGTTCTTTACAAATCATTTNNNNNNNNNNNNNNN^	<u>66</u>
F-TevII	Bacteriophage T4	5'-TTTAATCCTCGCTTC^AGATATGGCAACTG 3'-AAATTAGGAGCGA^AGTCTATACCGTTGAC	<u>67</u>
H-Drel	<i>E. coli pl-Drel</i>	5'-CAAAACGTCGTAA^GTTCCGGCGCG 3'-GTTTTGCAG^CATTCAAGGCCGCGC	<u>68</u>
I-BasI	<i>Bacillus thuringiensis phage Bastille</i>	5' AGTAATGAGCCTAACGCTCAGCAA 3'- TCATTACGAGTCGAACTCGGATTG	<u>69</u> <u>70</u>
I-Bmol	<i>Bacillus mojavensis</i> s87-18	5'-GAGTAAGAGCCCG^TAGTAATGACATGGC 3'-CTCATTCTCG^GGCATCATTACTGTACCG	<u>71</u>
I-PogI	<i>Pyrobaculum oguniense</i>	5'-CTTCAGTAT^GCCCCGAAAC 3'-GAAGT^CATACGGGGCTTTG	<u>72</u>
I-TwoI	<i>Staphylococcus aureus</i> phage <i>Twort</i>	5'-TCTTGACCTACACAATCCA 3'-AGAACGTGGATGTGTTAGGT	<u>73</u>
PI-Mgal	<i>Mycobacterium gastri</i>	5'-CGTAGCTGCCCAGTATGAGTCA 3'-GCATCGACGGGTCATACTCAGT	<u>74</u>
PI-PabI	<i>Pyrococcus abyssi</i>	5'-GGGGGCAGCCAGTGGTCCCGTT 3'-CCCCCGTCGGTCACCAGGGCAA	<u>75</u>
PI-PabII	<i>Pyrococcus abyssi</i>	5'-ACCCCTGTGGAGAGGAGCCCCTC 3'-TGGGGACACCTCTCCTCGGGGAG	<u>76</u>

In the specification at page 89 line 1, please replace the paragraph starting with "Fig.: 12" with the following amended paragraph:

Fig.: 12 Alignment of the catalytic site of various D-amino acid oxidases

Multiple alignment of the catalytic site of various D-amino acid oxidases allows for determination of a characteristic sequence motif [LIVM]-[LIVM]-H*-[NHA]-Y-G-x-[GSA]-[GSA]-x-G-x₅-G-x-A (SEQ ID NO: 17), which allows for easy identification of additional D-amino acid oxidases suitable to be employed within the method and DNA-constructs of the invention.

In the specification at page 90 line 32, please replace the paragraph starting with "The yeast" with the following amended paragraph:

The yeast *R. gracilis* was grown in liquid culture containing 30 mM D-alanine to induce *daol*, the gene encoding DAAO. Total RNA was isolated from the yeast and used for cDNA synthesis.

The PCR primers

5'-ATTAGATCTTACTACTCGAAGGACGCCATG-3' (SEQ ID NO: 77) and

5'-ATTAGATCTACAGCCACAATTCCCGCCCTA- 3' (SEQ ID NO: 78)